

SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> 311/0003

<140> 2 302 861

<141> 2000-04-10

<160> 28

<170> PatentIn version 3.0

<210> 1

<211> 141

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(141)

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gat	gaa	tta	gag	att	atc	att	ggc	gga	agc	gga	agc	cta	tca	aca	ttt	96
Asp	Glu	Leu	Glu	Ile	Ile	Ile	Gly	Gly	Ser	Gly	Ser	Leu	Ser	Thr	Phe	
			20				25					30				

ttc	cgg	ctg	ttt	aac	aga	agt	ttt	aca	caa	gct	ttg	gga	aaa	taa	141
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<212> PRT

<213> Streptococcus mutans

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Sub
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0983301-04001

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
20 25 30

tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
85 90 95

ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336

325

330

335

atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat 1056
Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc 1104
Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc 1152
Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc 1200
Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att 1248
Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
405 410 415

ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat 1296
Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
420 425 430

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<212> PRT

<213> Streptococcus mutans

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20 25 30

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

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090304.04.001

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Leu	Phe	Arg	Arg	Ala	Ile	Ile	Phe	Phe	Ile	Leu	Asp	Gly	Thr	Gln	Gly				
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Ile	Val	Met	Gly	Ser	Ser	Ile	Ile	Thr	Thr	Tyr	Met	Ile	Glu	Phe	Ala				
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Gly	Ile	Ala	Leu	Ser	Tyr	Leu	Phe	Leu	Ser	Val	Phe	Asn	Val	Asp	Ile				
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Leu	Tyr	Val	Ile	Glu	Ser	Tyr	Asn	Val	Ile	Pro	Thr	Leu	Lys	Phe	Arg				
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Lys	Phe	Val	Val	Ile	Val	Tyr	Leu	Ile	Leu	Phe	Leu	Ile	Leu	Ile	Ser				
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Phe	Leu	Ser	Gln	Tyr	Thr	Lys	Gln	Lys	Val	Gln	Asn	Glu	Ile	Met	Ala				
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Gln	Lys	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Thr	Gln	Tyr	Ser	Gln	Gln	Ile				
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Glu	Ser	Leu	Tyr	Lys	Asp	Ile	Arg	Ser	Phe	Arg	His	Asp	Tyr	Leu	Asn				
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Ile	Leu	Thr	Ser	Leu	Arg	Leu	Gly	Ile	Glu	Asn	Lys	Asp	Leu	Ala	Ser				
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Ile	Glu	Lys	Ile	Tyr	His	Gln	Ile	Leu	Glu	Lys	Thr	Gly	His	Gln	Leu				
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Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
405 410 415

Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
420 425 430

Leu Phe Lys Gln Leu Leu Ile Ile Lys
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<212> DNA

<213> Streptococcus mutans

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<222> (1)..(750)

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FOOTNOTES

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ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat	96
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr	
20 25 30	
aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc	144
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile	
35 40 45	
cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa	192
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys	
50 55 60	
aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat	240
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His	
65 70 75 80	
aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg	288
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met	
85 90 95	
ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa	336
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys	
100 105 110	
tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat	384
Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr	
115 120 125	
tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt	432
Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe	
130 135 140	
att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att	480
Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile	
145 150 155 160	
ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act	528
Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr	
165 170 175	
tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa	576
Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys	
180 185 190	
atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct	624
Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro	
195 200 205	
gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga	672
Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg	

210 215 220
aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga 720
Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
225 230 235 240

gct gtg att gct gat caa agg aga gca aaa 750
Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
245 250

<210> 6

<211> 250

<212> PRT

<213> Streptococcus mutans

<400> 6

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1 5 10 15

Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
20 25 30

Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
35 40 45

Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
50 55 60

Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
65 70 75 80

Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
85 90 95

Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
100 105 110

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
210 215 220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
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Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys

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<213> Streptococcus mutans

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<222> (1) .. (46)

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1				5					10					15	

Asp	Glu	Leu	Glu	Ile	Ile	Ile	Gly	Gly	Ser	Gly	Ser	Leu	Ser	Thr	Phe
			20					25						30	

Phe	Arg	Leu	Phe	Asn	Arg	Ser	Phe	Thr	Gln	Ala	Leu	Gly	Lys
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<212> PRT

<213> Streptococcus mutans

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<222> (1) .. (46)

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1				5					10					15	

Asp	Glu	Leu	Glu	Ile	Ile	Ile	Gly	Gly	Ser	Gly	Ser	Leu	Ser	Thr	Phe
			20					25					30		

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T00T10"2T0EE660

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
 35 40 45

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<212> PRT

<213> Streptococcus mutans

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<222> (1)..(43)

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
 1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe
 20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala
 35 40

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<212> PRT

<213> Streptococcus mutans

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<222> (1)..(46)

<400> 11

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
 20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

<210> 12

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<212> PRT

<213> Streptococcus mutans

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<222> (1) .. (46)

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<212> PRT

<213> Streptococcus mutans

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<222> (1) .. (46)

<400> 13

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe

Sub
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FOOTNOTES

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<213> synthetic construct

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Gln Ala Leu Gly Lys
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<210> 15

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<212> DNA

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19

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<213> synthetic construct

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<222> (1) .. (20)

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<210> 17

<211> 24

<212> DNA

<213> synthetic construct

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<222> (1) .. (24)

<400> 17

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24

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<212> DNA

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<222> (1) .. (21)

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<222> (1) .. (22)

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Sub
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093301 04401

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- <211> 480
- <212> DNA
- <213> Streptococcus mutans

- <220>
- <221> CDS

<222> (1) .. (408)

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tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438
Glu Leu Phe Glu Arg Leu Val Ala
130 135

ctgaaagatt tacgtaaaaa attaatgat ttttaaggaaa aa 480

<210> 23

<211> 136

<212> PRT

<213> Streptococcus mutans

<400> 23

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val

1 5 10 15
 Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
 20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
 35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
 50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
 65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
 85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
 100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
 115 120 125

Glu Leu Phe Glu Arg Leu Val Ala
 130 135

<210> 24

<211> 680

<212> DNA

<213> Streptococcus mutans

<220>

<221> misc_feature

<222> (1)..(680)

<400> 24

gtaaataaaa cagccagtta agatgggaca tttatgtcct gttcttaaag tctttttcgt 60

tttataataa ttttattata aaaggaggtc atcgtaatag atggaagaag attttgaaat 120

tgtttttaat aagggttaagc caattgtatg gaaattaagc cgttattact ttattaaaat 180
 gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaagggg 240
 acatcagaa ttagaagagg atgatacaaa attgtatatc tattttaaga cacgtttttc 300
 taattacatt aaagatgttt tgcgtcagca agaaagtcag aaacgtcgtt ttaatagaat 360
 gtcttatgaa gaagtcggtg agattgaaca ctgtttgtca agtggcggta tgcaattgga 420
 tgaatatatt ttatttcgtg atagtttgct tgcataataa caaggtctga gtactgaaaa 480
 gcaagagctg tttgagcgtg tggtagcagg agagcacttt ttgggaaggc aaagtatgct 540
 gaaagattta cgtaaaaaat taagtgattt taaggaaaaa tagttaaaaa gggaaagaat 600
 ggaacatgtg attgtaccat tcttttttgg tgaaaattaa gaaaagttat tataaattat 660
 tggtttaaca tgccatatta 680

<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(2280)

<400> 25
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 Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
 1 5 10 15
 ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
 Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
 20 25 30
 tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
 Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45
 cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
 His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60

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FOOTNOTES 240-240

gtg	ctg	gca	tct	gtt	gca	aag	cat	tac	gga	tct	aat	tac	tct	atc	gct	240
Val	Leu	Ala	Ser	Val	Ala	Lys	His	Tyr	Gly	Ser	Asn	Tyr	Ser	Ile	Ala	
65					70				75					80		
tat	ctg	cgg	gaa	ctc	tca	aag	act	aac	aag	cag	gga	aca	aca	gct	ctt	288
Tyr	Leu	Arg	Glu	Leu	Ser	Lys	Thr	Asn	Lys	Gln	Gly	Thr	Thr	Ala	Leu	
			85					90						95		
ggc	att	gtt	gaa	gct	gct	aaa	aag	tta	ggc	ttt	gaa	aca	cgc	tct	atc	336
Gly	Ile	Val	Glu	Ala	Ala	Lys	Lys	Leu	Gly	Phe	Glu	Thr	Arg	Ser	Ile	
			100					105					110			
aag	gcg	gat	atg	acg	ctt	ttt	gat	tat	aat	gat	ttg	acc	tat	cct	ttt	384
Lys	Ala	Asp	Met	Thr	Leu	Phe	Asp	Tyr	Asn	Asp	Leu	Thr	Tyr	Pro	Phe	
		115					120					125				
atc	gtc	cat	gtg	att	aaa	gga	aaa	cgt	ctg	cag	cat	tat	tat	gtc	gtc	432
Ile	Val	His	Val	Ile	Lys	Gly	Lys	Arg	Leu	Gln	His	Tyr	Tyr	Val	Val	
	130				135					140						
tat	ggc	agc	cag	aat	aat	cag	ctg	att	att	gga	gat	cct	gat	cct	tca	480
Tyr	Gly	Ser	Gln	Asn	Asn	Gln	Leu	Ile	Ile	Gly	Asp	Pro	Asp	Pro	Ser	
145				150						155					160	
gtt	aag	gtg	act	agg	atg	agt	aag	gaa	cgc	ttt	caa	tca	gag	tgg	aca	528
Val	Lys	Val	Thr	Arg	Met	Ser	Lys	Glu	Arg	Phe	Gln	Ser	Glu	Trp	Thr	
			165					170						175		
ggc	ctt	gca	att	ttc	cta	gct	cct	cag	cct	aac	tat	aag	cct	cat	aaa	576
Gly	Leu	Ala	Ile	Phe	Leu	Ala	Pro	Gln	Pro	Asn	Tyr	Lys	Pro	His	Lys	
			180					185					190			
ggt	gaa	aaa	aat	ggt	ttg	tct	aat	ttc	ttc	cgc	ttg	atc	ttt	aag	cag	624
Gly	Glu	Lys	Asn	Gly	Leu	Ser	Asn	Phe	Phe	Pro	Leu	Ile	Phe	Lys	Gln	
		195					200					205				
aaa	gct	ttg	atg	act	tat	att	atc	ata	gct	agc	ttg	att	gtg	acg	ctc	672
Lys	Ala	Leu	Met	Thr	Tyr	Ile	Ile	Ile	Ala	Ser	Leu	Ile	Val	Thr	Leu	
	210					215					220					
att	gat	att	gtc	gga	tca	tac	tat	ctc	caa	gga	ata	ttg	gac	gag	tac	720
Ile	Asp	Ile	Val	Gly	Ser	Tyr	Tyr	Leu	Gln	Gly	Ile	Leu	Asp	Glu	Tyr	
225				230						235					240	
att	cct	gat	cag	ctg	att	tca	act	tta	gga	atg	att	acg	att	ggt	ctg	768
Ile	Pro	Asp	Gln	Leu	Ile	Ser	Thr	Leu	Gly	Met	Ile	Thr	Ile	Gly	Leu	
			245						250					255		
ata	ata	acc	tat	att	atc	cag	cag	gtc	atg	gct	ttt	gca	aaa	gaa	tac	816
Ile	Ile	Thr	Tyr	Ile	Ile	Gln	Gln	Val	Met	Ala	Phe	Ala	Lys	Glu	Tyr	
			260					265					270			
ctc	ttg	gcc	gta	ctc	agt	ttg	cgt	tta	gtc	att	gat	gtt	atc	ctg	tct	864
Leu	Leu	Ala	Val	Leu	Ser	Leu	Arg	Leu	Val	Ile	Asp	Val	Ile	Leu	Ser	
		275					280					285				
tat	atc	aaa	cat	att	ttt	acg	ctt	cct	atg	tct	ttc	ttt	gcg	aca	agg	912

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
 290 295 300
 cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att 960
 Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
 305 310 315 320
 gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg 1008
 Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
 325 330 335
 gta att ttg gtt ggt ggg gtt ttg ttg gcg caa aac aat aac ctt ttc 1056
 Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
 340 345 350
 ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct 1104
 Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
 355 360 365
 ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat 1152
 Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
 370 375 380
 gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc 1200
 Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
 385 390 395 400
 att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt 1248
 Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
 405 410 415
 gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt 1296
 Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
 420 425 430
 gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt 1344
 Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445
 gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca 1392
 Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460
 gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat 1440
 Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480
 cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc 1488
 Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495
 gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt 1536
 Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510
 gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att 1584
 Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile

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FOOTNOTES

515

520

525

tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta 1632
 Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
 530 535 540

tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt 1680
 Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
 545 550 555 560

gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat 1728
 Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
 565 570 575

ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta 1776
 Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
 580 585 590

aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg 1824
 Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
 595 600 605

caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta 1872
 Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
 610 615 620

gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa 1920
 Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
 625 630 635 640

att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag 1968
 Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
 645 650 655

aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg 2016
 Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
 660 665 670

att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg 2064
 Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
 675 680 685

gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc 2112
 Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
 690 695 700

agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac 2160
 Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
 705 710 715 720

cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag 2208
 Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
 725 730 735

gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa 2256
 Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
 740 745 750

ggt ttc tat tat aac ctg ttt aat
 Gly Phe Tyr Tyr Asn Leu Phe Asn
 755 760

2280

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
 1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
 20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
 65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
 85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
 100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
 115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
 130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
 145 150 155 160

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B.

09833017-041001

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile ~~Lys~~ Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn ~~Leu~~ Gln Ser Lys Leu Gln Ser Ala Arg
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser ~~Lys~~ Val Ser Leu Val
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys ~~Leu~~ Ile Val Asn
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu

61

610

615

620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 27

<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1) .. (900)

<400> 27

atg gat cct aaa ttt tta caa agt gca gaa ttt tat agg aga cgc tat 48
Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
1 5 10 15

cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc 96
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att 144
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct 192
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct 240
Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65 70 75 80

gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca 288
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
85 90 95

aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga 336
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
100 105 110

gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag 384
Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
115 120 125

tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac 432
Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
130 135 140

aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att 480
Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145 150 155 160

ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt 528
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
165 170 175

gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat 576
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
180 185 190

att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat 624
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa 672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act 768
Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

atg aca ggc aag ~~aca~~ gtc act gtc att gat aaa aag act tat ttt gat 864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

tat ttc aaa gat aaa tta ctg cat aaa atg gat aat	900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn	
290 295 300	

<213> Streptococcus mutans

Met Asp Pro Lys Phe Leu Gln Ser Ala ~~Glu~~ Phe Tyr Arg Arg Arg Tyr
1 5 10 15

His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65 70 75 80

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
85 90 95

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B

[illegible]

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
100 105 110

Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
290 295 300